



Genetic Syndromes as a Cause of Obesity in Saudi Paediatric Population - A Narrative Review

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Abstract Childhood obesity remains one of the most significant health issues worldwide, affecting over 340 million individuals around the world. Research indicates that childhood obesity is prevalent in at least 1.8 per 1000 live births in Saudi Arabia. The genetic disposition greatly influences obesity in these nations as can be inferred from twin studies and identification of rare monogenic obesity types. Obesity is a multifaceted characteristic arising from an intricate interplay of contributing factors, including genetic and environmental influences, that collectively elevate the risk of disease. Inactive lifestyles and calorie-rich diets are significant environmental contributors to the obesity epidemic. The genetics of childhood obesity differs in particular ways from the genetics of adult obesity. Adult obesity and its associated disorders have been known to be correlated to childhood BMI. Among the childhood obesity syndromes, Prader Willi and Bardet Biedl syndromes are among the most well-known. Thus, this review discusses about the highlights of obesity related genetic syndromes and their prevalence in the population of Saudi Arabia.

Key Words Genetic Syndromes, Obesity, Saudi Arabia, Childhood obesity, Children

INTRODUCTION

With over 340 million cases documented worldwide in 2017, childhood obesity can be considered a major global health concern [1]. Sedentary lifestyle and heightened intake of fat-rich foods linked to enhanced living conditions has led to the rise of childhood obesity in Arab countries significantly [2]. Research indicates that childhood obesity is prevalent in at least 1.8 per 1000 live births in Saudi Arabia [3,4]. The genetic disposition greatly influences obesity in these nations as can be inferred from twin studies and identification of rare monogenic obesity types [5,6]. Currently, it is considered that obesity is a complicated and multifaceted condition that is produced by a number of interactions that involve numerous elements. These interactions include multiple factors, such as metabolic, environmental, behavioural, cultural, economic, sociodemographic and genetic aspects [7].

Obesity is a multifaceted condition arising from the interaction of contributory components, comprising of genomic and environmental elements, which collectively contribute to the development of the disease [8]. High-calorie consumption and sedentary lifestyle are substantial environmental factors that influence the obesity epidemic.

The genetic factors influencing childhood obesity are distinct from those affecting adult obesity [9,10]. The combined effects environment and genes undergo a substantial transformation from birth to maturity and are influenced by sex-specific factors. The progression of BMI is especially vital in infancy stages from 0.5 to 1.5 years and from 5 to 6. During this phase, the trajectory of BMI is established [11]. Later, the dynamic function of differential genetic expression of obesity due to age gets further complicated by sex-specific genetic effects [9].

Adult adiposity and its associated problems have been linked with childhood BMI [12,13]. The Middle East region possesses the biggest dietary energy surplus among emerging nations, which is linked with an alarming rise in risk factors for noncommunicable diseases, especially obesity [14]. A systematic review of 76 variants identified 76 variations inside or next to 49 genes that are significantly related with obesity, based on a cohort of 15,488 Arab cases and 9,760 controls. 19 of the 76 variants were identified as linked with obesity in Arab populations, but not in non-Arab groups, while two were characterized as exclusive to Arabs [15]. Similarly, 13 findings from a recent systematic review

conducted in 2022 identified 30 more cases of severe early-onset of obesity. 14 variants in five genes (LEP, LEPR, POMC, MC4R and CPE) were identified during the study. These pathogenic, homozygous variants were found in members of consanguineous families [16].

Genetic variants of obesity, although displaying a range of clinical characteristics, have traditionally been divided in three specific subtypes: Mendelian (monogenic) syndromic obesity, Mendelian non-syndromic obesity and polygenic obesity [17]. Pleiotropic syndromes, often known as syndromic variants of Mendelian obesity, are comparatively uncommon in the general population. Syndromic obesity is defined as obesity with particular characteristics, such as dysmorphic traits, congenital defects and intellectual disability that affects certain organ systems and Prader-Willi and Bardet-Biedl remain two of the most recognized obesity syndromes [18,19]. Access to accurate regional information, including epigenetic trends and credible national genetic data is crucial for a region-wise initiative to tackle the mounting problem of genetic origins of childhood obesity. Thus, our review discusses about the highlights of genetic syndromes related to obesity and their prevalence on Saudi population.

Genetic Syndromes and Obesity

A few genetic syndromes that are associated with obesity are as follows:

Monogenic Obesity Syndromes

Bardet-Biedl Syndrome (BBS)

Georges Bardet and Arthur Biedl identified BBS as a rare autosomal recessive disorder. It results in defects in multiple organ systems throughout the body and therefore, multisystemic in nature. This pleiotropic ciliopathy is defined by 6 primary characteristics, which include postaxial polydactyly, truncal obesity, hypogenitalism, retinal degeneration, renal abnormalities and mental disability, as evidenced by their prevalence in the patient population [20,21]. Obesity ranks as the second most common trait of BBS, impacting 72-92% of individuals diagnosed with the condition. The BMI for females and males have been reported to be 31.5 and 36.6 mg/m², respectively [22]. It typically shows itself in childhood and tends to grow more severe with age. The physiological approaches show that obesity can originate from either centre or the periphery. At the molecular level, it has been found that the overexpression of Tumor Necrosis Factor (TNF) α in the adipose and muscle tissues significantly contributes to insulin resistance in the context of immune response-mediated obesity. The vital contribution of the inflammatory immune response in obesity is highlighted by the role of TNF α as a primary mediator of this response [24].

Alström Syndrome (ALMS)

ALMS, an extremely rare genetic disorder, occurs in approximately one in a million individuals, due to pathogenic

variations in the ALMS1 gene which is located on chromosome 2p13, comprising of 23 exons and encoding a predicted protein weighing 461.2 kDa with 4169 amino acids [25]. Detecting ALMS proves challenging due to presence certain characteristics at birth while others manifest as the child matures. Significant variation exists both intra- and inter-familiarily. Children with ALMS typically exhibit prominent phenotypes such as sensorineural hearing loss, infant cone-rod retinal dystrophy that can lead to insulin resistance, obesity and juvenile blindness. Common findings include infantile transient cardiomyopathy, deafness, type 2 diabetes mellitus (T2DM), infantile transient cardiomyopathy, systemic fibrosis, early childhood obesity with hyperphagia, progressive renal or liver dysfunction and insulin resistance. The transportation of glucose is regulated by ALMS1 via the actin cytoskeleton, that becomes crucial for insulin-stimulated GLUT4 transport [26]. Abosabie et al in 2024 conducted a systematic review in 2024 and found that ALMS1 gene's molecular genetic assessment is essential for confirming the diagnosis, offering conclusive clarity within the complex clinical presentation [27].

Cohen Syndrome

The detection of Cohen syndrome' is done through medical observations or by detecting presence of pathogenic allelic variations in VPS13B (also known as COH1) through molecular genetic testing when clinical manifestations are ambiguous [28]. This is an autosomal recessive genetic disorder caused by a defective gene situated on chromosome 8 at 8q22-q23. Cohen syndrome is marked by the development of truncal obesity and a failure to thrive during childhood in more than 80% of affected adolescents [29]. The mean age at which obesity begins is 11.3 years. Reports indicate a swift transformation occurring within a span of 4-6 months, despite the absence of notable alterations in appetite, dietary consumption, or physical activity [30].

Carpenter Syndrome (CRPTS)

CRPTS is an autosomal recessive disorder identified primarily by and craniosynostosis and polysyndactyly of the feet and hand. Additional characteristics that have been reported include cryptorchidism, congenital heart disease and obesity [31]. CRPT, present in around 1 in 1 million births, is marked by obesity, polydactyly, heart abnormalities and craniosynostosis [32,33]. CRPTS is classified into 2 distinct types. Carpenter syndrome-1 (CRPT1) is caused by homozygous mutations in the RAB23 gene [34]. The Human Gene Mutation Database (HGMD) indicates that individuals with CRPT1 have been recorded to have only 17 pathogenic RAB23 variants [35]. Carpenter Syndrome-2 (CRPT2) is primarily caused due to mutations in the MEGF8 gene [36].

Albright's Hereditary Osteodystrophy (AHO)

Initial findings on AHO reported a child with a rounded facial structure, abbreviated metacarpals and metatarsals, along with

multiple regions of soft tissue ossification and a short, stocky physique [37]. 50-65% of individuals with AHO, even with normal or low birth weights were reported to have generalized obesity. Although the exact causes of obesity remain unknown, multiple potential mechanisms may be at play [38]. G-proteins transduce the melanocortin receptor (MC4R), which is identical to many other G-protein-coupled seven transmembrane receptors which transmit anorexigenic signals from hormones and other neurotransmitters. Mutations in this receptor were among the most common causes of genetic obesity. This lack of anorexigenic signals, particularly those involving MC4R, is believed to lead to hyperphagia; nonetheless, this occurrence is yet to be fully investigated in obese AHO individuals [39].

Rubinstein-Taybi Syndrome(RSTS)

RSTS is a multisystem disorder marked by distinct physical, cognitive and behavioural features. It is named after US paediatrician Jack Rubinstein and Iranian radiologist Hooshang Taybi, who reported on seven affected infants in 1963 [40]. It potentially arises from variations in 2 genes that regulate transcription via chromatin remodelling. This disorder is marked by presence of dysmorphic features, such as broad toes, broad thumbs and clinodactyly. In certain instances, obesity may also present itself during childhood and adolescence. Approximately 90% of individuals with RSTS attain adulthood despite the need for costly and specialised clinical treatment. After the patients reach adulthood, RSTS is marked by mental and behavioural health disorders (83%), insomnia (62%) and gastrointestinal issues like constipation being the most prevalent (73%) [41]. In the 1990s, the molecular basis of RSTS was first reported when deletions in 16p13 region of chromosome 16 were observed in affected patients, which subsequently led to identification of pathogenic variations in CREBBP gene [42]. RSTS can be categorized into two main variations, both showing autosomal dominance. RSTS type 1 is caused by deletions or pathogenic variants in the CREBBP gene and accounts for roughly 50-60% of RSTS cases. RSTS type 2 makes up about 8-10% of RSTS cases and is associated with pathogenic variations in the EP300 gene [43-46].

Obesity Syndromes with Chromosomal and Imprinting Anomalies

A number of additional chromosomal syndromes, particularly deletions of chromosomes, have been discovered in conjunction with obesity. Obesity is typically developed in patients who carry these syndromes, but this is not always the case. In light of this, it is possible that the development of obesity requires either penetrance or variable expression levels. The following syndromes are included, but not limited to: 11p13 (WAGR syndrome), 1p36 (monosomy 1p36 syndrome), 9q34 (Kleefstra syndrome), 17p11.2 (Smith-Magenis syndrome), 6q16 (PWS-like syndrome) and 2q37 (brachydactyly mental retardation syndrome; BDMR).

In these certain genes, haploinsufficiency is likely to account for specific observed phenotypes [47]. A few of them are as follows:

Prader-Willi Syndrome (PWS)

PWS is recognized as the most prevalent genetic cause of obesity, reported in about 1 in 10,000 to 1 in 30,000 live births [48,49]. PWS is caused due to the absence of expression of genes that are derived from the father in the critical region of the PWS gene, situated on chromosome 15q11-q13. Approximately 65-70% of the observed cases are attributed to the deletion of this region (type 1 or type 2, depending on the proximal break point). 20-30% of the cases are due to a maternal uniparental disomy of chromosome 15 and the majority of the remaining two percent to five percent have an imprinting center defect or unbalanced translocations (about one percent) [50,51]. PWS is a complex multisystem disorder marked by short stature, behavioral issues, short stature, psychiatric disorders, feeding difficulties in early infancy, neonatal hypotonia, cognitive deficits and distinctive physical characteristics (prominent facial features, scoliosis, reduced hand and foot size and narrow hands with a straight ulnar border). It also involves various endocrine disorders (growth hormone [GH]/insulin-like growth factor-I axis dysfunction, hypogonadism, central adrenal insufficiency, hypothyroidism), early onset of hyperphagia with food-seeking behavior leading to severe obesity if dietary intake remains unchecked [52]. A complex dysregulation of the hypothalamus is presently believed to account for the PWS phenotype [53]. From ages 1 to 6, Mild obesity begins about 1 year of age, with hyperphagia and severe obesity often manifesting between ages 2 and 6. In the absence of suitable dietary restrictions, environmental management and behavioral interventions, obesity advances into adulthood, resulting in obesity-related health issues, including chronic leg edema, thrombophlebitis, T2DM, cardiopulmonary disease and mortality before the age of 35 [54] According to Rahman *et al.* [55], the probable causes of hyperphagia include hormonal anomalies, which involve elevated levels of leptin and ghrelin from infancy to adulthood. At certain ages, hormone levels in the thyroid, insulin and peptide YY decreased. In individuals ranging from 4 to 30 years old, neuronal abnormalities linked to Orexin A and changes in brain structure were found.

Deletion 6q16

Prior research has linked interstitial deletion of chromosome 6q16 to a PWS like phenotype, characterized by shortened extremities, hypotonia, developmental delay and obesity. In instances of obesity, recognized candidate genes have been detected within significant genomic intervals such as SIM1 (6q16) and BDNF (11p13) [56]. Children with deletions exhibit strabismus, a thin upper lip, almond-shaped eyes, hypogonadism, learning disabilities, microretrognathia, developmental delays, small hands and feet, hypotonia,

behavioral issues, cerebellar signs and neonatal feeding difficulties, presenting similarities with characteristics observed in PWS [57].

Deletion 1p36

Monosomy 1p36, also known as 1p36 deletion syndrome, is a subtelomeric monosomy occurring in 1 in every 5000 births. The primary clinical characteristics of this syndrome encompass hypotonia and motor developmental delay, accompanied by craniofacial dysmorphisms and short stature, including prominent forehead and chin, deep-set eyes, large anterior fontanel, a flat nasal bridge, ear asymmetry and maxillary hypoplasia [58,59]. It was reported in a 9 year old with generalized obesity, who had a BMI above the 95th percentile, along with acanthosis nigricans on the arms and neck. The child also had broad nasal bridge, deep-set eyes, straight eyebrows, self-inflicted lesions and a pointed chin. Cytogenetic analysis revealed a deletion at 1p36.33-pter [60]. A different investigation revealed that obesity as a result of hyperphagia was present in two patients with mosaic deletions of 1p36, suggesting that those with 1p36 deletions may be susceptible to hyperphagia and obesity when both of the subsequent risk factors; deletions that cover 2-3 Mb critical region and less severe phenotypes that lead to overeating due to independent access to food are present [61].

Deletion 2q37

Deletions of distal 2q37 area comprise of terminal cytogenetic band on the long arm of chromosome 2, separated into three sub bands: 2q37.1, 2q37.2 and 2q37.3. In previous studies, deletions have been recorded in 4,115 patients, with clinical associations to obesity, brachydactyly, short stature and intellectual deficiency, collectively termed Albright's hereditary osteodystrophy-like syndrome [62]. Their features often include deep-set eyes, sparse hair, a round face, a bulbous nasal tip and thin lip borders. Numerous individuals experience seizures alongside mild cognitive impairment, with obesity occasionally observed [63].

Deletion 9q34.3

Most patients had sub-microscopic deletions in the subtelomeric region of chromosome 9q34.3, which ranged from less than 400kb to more than 3Mb [64]. Commonly observed characteristics include early-onset obesity accompanied by hyperphagia (Occurring in 2 to 3 years of age), significant developmental delay, intellectual disability, distinctive facial features (such as synophrys, brachycephaly, prognathism, anteverted nostrils and a thin upper lip), a neonatal hypotonia, syndactyly of toes, short neck and limbs, abnormal genitalia including micropenis, hypospadias, cryptorchidism, stereotypic hand movements, abnormal sleep with recurrent nocturnal awakenings and diminished attention span [65-67].

X-Linked Obesity Syndromes

Fragile X Syndrome (FXS)

Obesity is a prevalent issue in FXS, attributed to the molecular similarities between obesity-related disorders, notably PWS [63]. FXS results from a CGG expansion exceeding 200 repeats in the 5' untranslated region of FXS mental retardation 1 (FMR1) gene [68]. Increased repetitions may lead to either a premutation (55 to 200 repeats) or a full mutation (over 200 CGG repeats) status. The methylation of the promoter region due to a full mutation can lead to minimal or absence of production of FMR1 mRNA and consequently a deficiency of the FMR1 protein [69]. A study comprising of 260 patients with FXS (198 males and 62 females) was conducted by the Fragile X Clinical and Research Consortium. It was discovered that weight of children and adolescents with FXS may exceed that of general population [70]. Raspa *et al.* [71] collected data from a national survey that included 884 families to evaluate the general health of both adults and children with FXS. Obesity prevalence among adults with FXS aligns closely with that of the general population, estimated at around 30%. Male children with FXS showed increased obesity rates (31%) in contrast to their normally developing counterparts of the same age (18%).

Börjeson-Forssman-Lehmann Syndrome (BFLS)

BFLS is a relatively rare X-linked disorder characterized by significant cognitive deficits, prominent fleshy ears, obesity with gynecomastia, hypogonadism and distinct facial morphology [72]. Individuals with BFLS generally show a normal birth weight; however, they demonstrate substantial truncal obesity by late childhood. Despite notable differences in obesity levels, individuals with reduced overall fat often display a fat distribution in the lower abdomen and hips in the same pattern as females. The Plant homeodomain finger gene 6(PHF6) has been identified as the gene that is altered in patients with BFLS [73]. The clinical history and physical examination of all affected males suggest that this phenotype exhibits a less severe yet more variable presentation than previously recorded, with changes observed with age [74].

Case Studies in Saudi Arabia

Research has shown a notable prevalence of obesity, especially in children, among the Saudi population, which demonstrates a high level of consanguinity. Consanguinity is particularly prevalent in many Arab nations, with rates ranging from 20 to 50% of all marriages [75]. Mohammed *et al.* [76]. conducted a systematic review in 2023 and explored genetic conditions leading to monogenic obesity in a cohort of 243 children from Qatar. In a study, thirty rare variants that may be associated with obesity were discovered in 36 of the 243 probands, representing 14.8%, across 15 candidate genes. Variants in the MC4R gene emerged as primary contributor to obesity, responsible for as much as 19% of cases.

Progress in genetics has enabled researchers to isolate mutations associated with the onset of BBS, namely the BBS1, BBS2, ARL6/BBS3, MKKS/BBS6, BBS7, TTC8/BBS8, B1/BBS9, BBS10 and TRIM32/BBS11 genes [77,78]. The prevalence of BBS genes mutations, particularly BBS3 and BBS9, have been observed in populations of Asian descent, such as those from Saudi Arabia and India, compared to other populations [79,80]. There exist numerous phenotypes of BBS that vary in disease severity, contingent upon the locus of the mutated gene, with most documented cases associated with mutations in different BBS genes [20]. In 2022, Alhamoud M et al. documented an instance of BBS in a five-year-old Saudi girl, who exhibited obesity subsequent to hypogonadism and polydactyly, among other symptoms. The child exhibited typical indicators of central obesity, characterized by a rounded facial appearance and dysmorphic traits. Genetic testing in the patient revealed the variant of uncertain significance c.1553-1G>A p.? likely in homozygosity within the BBS9 gene located on chromosome 7, demonstrating an autosomal recessive inheritance pattern, which supports our clinical diagnosis of BBS9 [81]. In 2024, Milibari et al. identified 46 individuals with BBS from 31 Saudi families, with obesity observed in 91% of the patients [82]. An increased prevalence of obesity among both children and adults was found in the clinical spectrum of 11 patients from four consanguineous families in Saudi Arabia in a study by Cherian and Al-Sanna'a [83].

Regional variations exist and the BBS4, BBS5 and BBS8 mutations were predominately present within patients from the Middle East specifically, North Africa, Kuwait and Saudi Arabia [83]. BBS4 had little effect on BBS, even though it is significantly more common in Arab families compared to white families in Europe and North America [21,84-88]. A concise methodology, grounded in the prevalence of pathogenic mutations, is necessary for the molecular diagnosis of BBS given its considerable heterogeneity.

A study involving 12 patients with ALMS, including 9 children, revealed genetic and medical heterogeneity; 6 of them exhibited a founder mutation (IVS18-2A>T in exon 19), while the remaining 6 exhibited private mutations [89]. Aldahmesh et al. [90] demonstrated that, regardless of population-level endogamy, a consanguineous union suffices to render a genomic area homozygous, directly correlating with the degree of consanguinity. Four novel alleles were identified, utilizing ALMS to demonstrate the significant phenomenon of allelic heterogeneity in a rare autosomal recessive disorder among a highly inbred Saudi population. It has been observed that with an average consanguinity rate of around 50%, individuals from Saudi Arabia are expected to have a considerably higher number of homozygosity blocks compared to many other populations. Bakar et al. [91] documented a case involving a 10-year-old girl from a clinic in Saudi Arabia, whose weight was positioned in the 80th percentile for her age group. Their emphasis was on the necessity for physicians to perform tests for ALMS when faced with a combination of obesity, diabetes, auditory

impairment and visual impairment. Consequently, ALMS in Saudi Arabia is likely undetected due to diverse medical presentations.

Mochida et al. [92] investigated Cohen syndrome in four populations and discovered that afflicted individuals in the Saudi Arabian lineage were homozygous for a novel mutation, 1219 C.T, in exon 9. This mutation converts a glutamine residue at position 407 of 4022 into a termination codon (Q407X), resulting in significantly truncated predicted protein. In a separate study, Hashmi et al. [93] examined a consanguineous Saudi family with three affected members. No distinct characteristics such as truncal obesity and musculoskeletal deformities, including hypotonia, were observed. However, in spite of the common symptoms, a definitive diagnosis of Cohen syndrome can only be established through genetic testing. Al-Qattan et al. [94] documented a case of RTS Type I in a 4-year-old Saudi boy, who was identified as heterozygous for a sequence variant c.4963del in the CREBBP gene, anticipated to cause premature protein termination. The child and his father were identified as heterozygous for the EP300 gene variant and anticipated to cause the amino acid substitution.

In the Al-Baha Region of Saudi Arabia, Al Ghamsi et al. [95] conducted a study involving 744 children and adolescents to outline the patterns and clinical outcomes associated with various non-diabetic pediatric endocrine disorders. Obesity was reported in 123 cases, accounting for 16.5%, whereas syndromes with endocrine characteristics were identified in 14 cases, representing 1.9%, which included 2 instances of PWS. Al Herbish et al. [96] identified that among 52 children referred to a tertiary health center in Riyadh for childhood obesity, 3 (5.8%) were diagnosed with PWS. A case involving an 8-year-old girl from Saudi Arabia has been documented, highlighting deletions on chromosome 1 at q31 and q42.1, along with congenital glaucoma present from birth. She exhibited bilateral buphthalmos with extensive opacities in the corneas and she was incapable of following or fixating on any directional gaze with either eye. Obesity was not identified as one of the symptoms [97]. Iqbal et al. [98] conducted an evaluation of the prevalence of FXTAS-positive cases within a cohort of 305 preselected individuals. In males, the FXTAS-positive cells ranged from 7% to 58%, whereas in females, it ranged from 14% to 21%. Al-Hur et al. [99] proposed a significant impact of consanguineous marriage on the frequency of FXTAS in the Eastern Region of Saudi Arabia. The assessment for related diseases demonstrated a direct correlation with rising rates in male instances with FXTAS. However, obesity was not a confounding factor in these cases.

CONCLUSION

The obesity pandemic can be attributed significantly to lifestyle changes that have occurred over the past three decades. Genetic testing validates clinical diagnosis and Genetic counselling are of utmost importance for early diagnosis in children and assist families dealing with genetic

obesity syndromes. Nevertheless, the prevalence of childhood obesity cannot be determined solely by the obesogenic environment; it must be accompanied by genetic predisposition. Unique disease susceptibility genotypes among Arabs are also significant contributing factors to obesity. In this review, some of the obesity-associated variations were also found in other ethnic, regional groups, but complicated gene-environment interactions enhance these genotypes, predisposing them to obesity. Consequently, the absence of genetic association studies focused on obesity within Arab populations highlights the necessity for more rigorously designed research and lack of longitudinal data to elucidate the genetic framework contributing to obesity potential in this particular population. Future research should focus on Conducting longitudinal studies on obesity progression in Saudi populations, investigating the genetic-environment interaction in obesity syndromes and exploring novel genetic mutations unique to the Arab population.

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